

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.

Application Serial Number: 09/855 340B  
Source: IFW/K  
Date Processed by STIC: 2-3-05

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 02/03/2005

PATENT APPLICATION: US/09/855,340B

TIME: 09:26:38

Input Set : A:\PTO.ST.txt

Output Set: N:\CRF4\02032005\I855340B.raw

```

3 <110> APPLICANT: Hosted, Jr., Thomas J.
4   Horan, Ann C.
6 <120> TITLE OF INVENTION: Isolation of Micromonospora carbonacea var africana
7   pMLP1 integrase and use of integrating function for
8   site-specific integration into Micromonospora
9   halophitica and Micromonospora carbonacea chromosome
11 <130> FILE REFERENCE: IN01164K
13 <140> CURRENT APPLICATION NUMBER: 09/855,340B
14 <141> CURRENT FILING DATE: 2001-05-15
16 <150> PRIOR APPLICATION NUMBER: 60/204,670
17 <151> PRIOR FILING DATE: 2000-05-17
19 <160> NUMBER OF SEQ ID NOS: 16
21 <170> SOFTWARE: PatentIn Ver. 2.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1179
25 <212> TYPE: DNA
26 <213> ORGANISM: Micromonospora carbonacea
28 <400> SEQUENCE: 1
29 gtgtggatcg agaagaacgg gcccggtctac cgcattcggg acctcgttcg cggtaaaaag 60
30 gtcaccattc agaccgggta tccgacgaag accagcgcca agaatgcgat ggtgcagttc 120
31 cgtgcgggagc agttgcaggg caacgcgctc atgccgcgcg gcggtcagat taccctcgcc 180
32 gatttcgtgg gggagtgggt gccgagctac gaaaagacgc tgaaaccgac cgccgtgaac 240
33 tcggagggca accgatccg caaccacctc ctgcccatac tcggccatct cacccttgac 300
34 gagctggacg ggcaggtcac ccagcagtggt gtcaacgacc tggaggccgg cgtcggccc 360
35 tggccggaggt ccacgcgggg tcgtcgggaag ccgctggcag cgaagacgat cagcaactgc 420
36 cacggcctgc tgcacacgat ctgcggcgcg gcgatcgcg cgaaacggat cagggtcaac 480
37 ccgtgctctt cgacgatgct gccccggcgc gagccgaaa agatgaagtt cctgagcgac 540
38 ccggagatcg gtcggcttat cacggcgctt ccgccgact ggcgaccgct cgtcatgctg 600
39 ctggtggcga ccggtctgag gtgggggtgag gcgatcggcc tgcgcgccgg ccgggtcgac 660
40 ctgctcgccg cgcgcccccg gctgaccgtc gtcgagcagc tccaggagct ggccagcacg 720
41 ggagagctcg tcttcagtc gccgaagacc gcgaagggcc ggcgacgggt cagtttcacc 780
42 acgaaagtcg ctctactgct tacgccactc atcgccggaa agaaaagtga cgaggtcgtg 840
43 ttcaccgcgc cgaaaggcgg gatggttaagg acgcgcaatt tccggcggat ctgggtcaag 900
44 gcgtgcgagg aagccggggt tccgggctta cgcattcacg atctgcggca cactcacgcg 960
45 gcgatcctga tttctgccgg gcgtccgctg tcggcgatct cccgcgcgct cggtcactcg 1020
46 tcgatcgcgg tcacggatct gctgtacggg cacctgcgtg aggaggtcga cgaggggatc 1080
47 ctgcgcggca tcgaggaggc gatggccggc gtccgggctg aggacctgga ggcggaactc 1140
48 gacgaggagc tgacggacgt gttggccgac gcagcatga 1179
51 <210> SEQ ID NO: 2
52 <211> LENGTH: 426
53 <212> TYPE: DNA
54 <213> ORGANISM: Micromonospora carbonacea
56 <400> SEQUENCE: 2

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57 atgcgcaaca caccggggct ggggcgcggc acatgggccg catacgtcct caccgcccgc 60
58 gagcgcgccg gactgaccaa gagcgagttg gccaggcgca tccagaagga ccggggccacc 120
59 gtcggcccggt gggaggacgg caagaaccgg cccgacgacg cggacctcgt tgcccgcgtc 180
60 gccacaggtgc tcggcctcga cctcgacgaa gccctcgccg ccgcaggtct gcgccccggc 240
61 gtcaccccgc cagcgacccc aaccatggac ctggacgagg aaatcgagct ggtccgcacc 300
62 gacccaagc tggacgagga catgaagcgg cgcatcatcg ccctaactct ggagcgccgt 360
63 gagcgcgaca aggcggcggc gatcgaggaa accaagcggc tcatcgacct gttccgcccg 420
64 agctga 426
67 <210> SEQ ID NO: 3
68 <211> LENGTH: 34
69 <212> TYPE: DNA
70 <213> ORGANISM: Micromonospora carbonacea
72 <400> SEQUENCE: 3
73 ccccggtacg ggttcaattc ccatcagtc cccg 34
76 <210> SEQ ID NO: 4
77 <211> LENGTH: 241
78 <212> TYPE: DNA
79 <213> ORGANISM: Micromonospora carbonacea
81 <400> SEQUENCE: 4
82 tattagtccg cagcgccccc ggccccgccg gagcggagcg catggtggct gtagctcagt 60
83 tggcagagca ccgggttgtg gtcccggttg tcgtgggttc aattcccatc agtcaccgcgt 120
84 acacgaaggc cccctccact cggagggggc cttcggcggt cctgagggtt cgcggtcagg 180
85 cggtcggtc ggcgctgggg gactcgccc cgtcggcggg agtggcctcg gcgtccgggg 240
86 a 241
89 <210> SEQ ID NO: 5
90 <211> LENGTH: 243
91 <212> TYPE: DNA
92 <213> ORGANISM: Micromonospora carbonacea
94 <400> SEQUENCE: 5
95 tggcgggggt gtggctatta ttagtccgca cgccgccggg ccccgccgga gcggagcgca 60
96 tgggtggtgt agctcagttg gcagagcacc gggttgtggt cccggttgct gtgggttcaa 120
97 ttcccatcag taccgcggca agtggtatcta ctccacagca gatcaggccc cctccgaaga 180
98 gggggcctga tgcgtcatag gggacaggta ggggaactca acccccggct ccttgctcgc 240
99 gtc 243
102 <210> SEQ ID NO: 6
103 <211> LENGTH: 247
104 <212> TYPE: DNA
105 <213> ORGANISM: Micromonospora carbonacea
107 <400> SEQUENCE: 6
108 taggggaatc cactccggag acgcccggag caatccggag catgacggag caaccagcag 60
109 gtcagggtgc ctgttgacct cctgaccagg gccccgttac gggttcaatt cccatcagtc 120
110 acccgtagac gaaggcccc tccactcgga gggggccttc ggcgttcctg agggttcgcg 180
111 gtcaggcggt cggctcggcg ctgggggact cgccccgctc ggcgggagtg gcctcggcgt 240
112 ccgggga 247
115 <210> SEQ ID NO: 7
116 <211> LENGTH: 255
117 <212> TYPE: DNA
118 <213> ORGANISM: Micromonospora halophytica
120 <400> SEQUENCE: 7

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```

121 tttctccgca cccgcccggg gcgttcgacc ggggtcggcg gcatggtggc ttagctcag 60
122 ttggcagagc accgggttgt ggtcccgggt gtcgtgggtt caattcccat cagtcacccc 120
123 aggtaagacc caggtcaggg ccggttctca ccggccctga cgcattttca ggggcatggt 180
124 gggggcgcta ccgggggtgg ggtgtctcac cgcgagccag catctcgatc aggcgatcga 240
125 gccggcgctg ccggg                                     255
128 <210> SEQ ID NO: 8
129 <211> LENGTH: 315
130 <212> TYPE: DNA
131 <213> ORGANISM: Micromonospora halophytica
133 <400> SEQUENCE: 8
134 tttctccgca cccgcccggg gcgttcgacc ggggtcggcg gcatggtggc ttagctcag 60
135 ttggcagagc accgggttgt ggtcccgggt gtcgtgggtt caattcccat cagtcacccc 120
136 gcaagtggat ctactccaca gcagatcagg cccctccga agagggggcc tgatgcgtca 180
137 taggggacag gtaggggaac tcaacccccg gctccttget cgcgtcgggt catgccgtcc 240
138 gcgtaccctt ccgcgtacct ggccctctcc cgttcctcga tctcggcggc gagctgatcg 300
139 cgcaggtgcg cctcc                                     315
142 <210> SEQ ID NO: 9
143 <211> LENGTH: 260
144 <212> TYPE: DNA
145 <213> ORGANISM: Micromonospora halophytica
147 <400> SEQUENCE: 9
148 taggggaatc cactccggag acgcccggag caatccggag catgacggag caaccagcag 60
149 gtcaggtggc ctgttgaccc cctgaccagg gccccggtac gggttcaatt cccatcagtc 120
150 accccaggtg agaccagggt cagggccggt tctcaccggc cctgacgcat tttcaggggc 180
151 atgggtgggg cgctaccggg ggtgggtgt ctcaccgcca gccagcatct cgatcaggcg 240
152 atcgagccgg cgctgccggg                                     260
154 <210> SEQ ID NO: 10
156 <211> LENGTH: 209
158 <212> TYPE: DNA
160 <213> ORGANISM: artificial sequence
164 <220> FEATURE:
166 <223> OTHER INFORMATION: pMLP1 attP region
168 <400> SEQUENCE: 10
169 taggggaatc cactccggag acgcccggag caatccggag catgacggag caaccagcag 60
171 gtcaggtggc ctgttgaccc cctgaccagg gccccggtac gggttcaatt cccatcagtc 120
173 acccggaag tgatctact ccacagcaga tcaggcccc tccgaagagg gggcctgatg 180
175 cgtcataggg gacaggtagg ggaactcaa                                     209
178 <210> SEQ ID NO: 11
180 <211> LENGTH: 19
182 <212> TYPE: DNA
184 <213> ORGANISM: artificial sequence
188 <220> FEATURE:
190 <223> OTHER INFORMATION: primer PR144
192 <400> SEQUENCE: 11
193 tgcttcgacg ccatcargg                                     19
196 <210> SEQ ID NO: 12
198 <211> LENGTH: 20
200 <212> TYPE: DNA
202 <213> ORGANISM: artificial sequence

```

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```

206 <220> FEATURE:
208 <223> OTHER INFORMATION: primer PR145
210 <220> FEATURE:
212 <221> NAME/KEY: misc_feature
214 <222> LOCATION: (7)..(7)
216 <223> OTHER INFORMATION: n is inosine (I)
220 <400> SEQUENCE: 12
W--> 221 gtggaanccg ccgaakccgc                                20
223 <210> SEQ ID NO: 13
225 <211> LENGTH: 20
227 <212> TYPE: DNA
229 <213> ORGANISM: artificial sequence
233 <220> FEATURE:
235 <223> OTHER INFORMATION: primer PDH504
237 <400> SEQUENCE: 13
238 agggcaacaa gggaagcgtc                                20
241 <210> SEQ ID NO: 14
243 <211> LENGTH: 21
245 <212> TYPE: DNA
247 <213> ORGANISM: artificial sequence
251 <220> FEATURE:
253 <223> OTHER INFORMATION: primer PDH505
255 <400> SEQUENCE: 14
256 ggcgggggtg tggctattat t                                21
259 <210> SEQ ID NO: 15
261 <211> LENGTH: 21
263 <212> TYPE: PRT
265 <213> ORGANISM: artificial sequence
269 <220> FEATURE:
271 <223> OTHER INFORMATION: amino acid sequence of open reading frame indicated in
figures 4b
272          and 4d
274 <400> SEQUENCE: 15
276 Ser Pro Asp Ala Glu Ala Thr Pro Ala Asp Gly Ala Glu Ser Pro Ser
277 1          5          10          15
280 Ala Glu Pro Thr Ala
281          20
284 <210> SEQ ID NO: 16
286 <211> LENGTH: 21
288 <212> TYPE: PRT
290 <213> ORGANISM: artificial sequence
294 <220> FEATURE:
296 <223> OTHER INFORMATION: amino acid sequence of open reading frame indicated in
figures 5b
297          and 5d
299 <400> SEQUENCE: 16
301 Arg Gln Arg Arg Leu Asp Arg Leu Ile Glu Met Leu Ala Arg Gly Glu
302 1          5          10          15
305 Thr Pro His Pro Arg
306          20

```

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/855,340B

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:12; N Pos. 7

**VERIFICATION SUMMARY**

DATE: 02/03/2005

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TIME: 09:26:39

Input Set : A:\PTO.ST.txt

Output Set: N:\CRF4\02032005\I855340B.raw

L:221 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0